

SEQUENCE LISTING



<110> French, Cynthia K.
Schneider, Patrick A.
Yamamoto, Karen K.

<120> Prostate Cancer-Specific Marker

<130> 107-206US-C

<140> 09/680,121

<141> 2000-10-04

<150> 60/041,246

<151> 1997-03-07

<150> 60/047,811

<151> 1997-05-15

<150> 09/036,315

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<150> 09/535,597

<151> 2000-03-27

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<170> PatentIn Ver. 2.1

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cgttccgaaa gccggcgctt gagatccagg caagtgaatc cagccaggca gttttccctt 120

cagcacctcg gacagaacac gcagtaaaaa atg gct ccg atc acc acc agc cgg 174
Met Ala Pro Ile Thr Thr Ser Arg

| | |
|---|-----|
| gaa gaa ttt gat gaa atc ccc aca gtg gtg ggg atc ttc agt gca ttt | 222 |
| Glu Glu Phe Asp Glu Ile Pro Thr Val Val Gly Ile Phe Ser Ala Phe | |
| 10 15 20 | |
| ggc ctg gtc ttc aca gtc tct ctc ttt gca tgg atc tgc tgt cag aga | 270 |
| Gly Leu Val Phe Thr Val Ser Leu Phe Ala Trp Ile Cys Cys Gln Arg | |
| 25 30 35 40 | |
| aaa tca tcc aag tct aac aag act cct cca tac aag ttt gtg cat gtg | 318 |
| Lys Ser Ser Lys Ser Asn Lys Thr Pro Pro Tyr Lys Phe Val His Val | |
| 45 50 55 | |
| ctt aag gga gtt gat att tac cct gaa aac cta aat agc aaa aag aag | 366 |
| Leu Lys Gly Val Asp Ile Tyr Pro Glu Asn Leu Asn Ser Lys Lys Lys | |
| 60 65 70 | |
| ttt gga gca gat gat aaa aat gaa gta aag aat aag cca gct gtg cca | 414 |
| Phe Gly Ala Asp Asp Lys Asn Glu Val Lys Asn Lys Pro Ala Val Pro | |
| 75 80 85 | |
| aag aat tca ttg cat ctg gat ctt gaa aag aga gat ctc aat ggc aat | 462 |
| Lys Asn Ser Leu His Leu Asp Leu Glu Lys Arg Asp Leu Asn Gly Asn | |
| 90 95 100 | |
| ttt ccc aaa acc aac ctc aaa cct ggc agt cct tct gat ctg gag aat | 510 |
| Phe Pro Lys Thr Asn Leu Lys Pro Gly Ser Pro Ser Asp Leu Glu Asn | |
| 105 110 115 120 | |
| gca acc ccg aag ctc ttt tta gaa ggg gaa aaa gag tca gtt tcc cct | 558 |
| Ala Thr Pro Lys Leu Phe Leu Glu Gly Glu Lys Glu Ser Val Ser Pro | |
| 125 130 135 | |
| gag agt tta aag tcc agc act tcc ctt act tca gaa gag aaa caa gag | 606 |
| Glu Ser Leu Lys Ser Ser Thr Ser Leu Thr Ser Glu Glu Lys Gln Glu | |
| 140 145 150 | |
| aag ctg gga act ctc ttc ttc tcc tta gaa tac aac ttc gag aga aaa | 654 |
| Lys Leu Gly Thr Leu Phe Phe Ser Leu Glu Tyr Asn Phe Glu Arg Lys | |
| 155 160 165 | |
| gca ttt gtg gtc aat atc aag gaa gcc cgt ggc ttg cca gcc atg gat | 702 |
| Ala Phe Val Val Asn Ile Lys Glu Ala Arg Gly Leu Pro Ala Met Asp | |
| 170 175 180 | |
| gag cag tcg atg acc tct gac cca tat atc aaa atg acg atc ctc cca | 750 |
| Glu Gln Ser Met Thr Ser Asp Pro Tyr Ile Lys Met Thr Ile Leu Pro | |

| | | | | |
|---|-----|-----|-----|------|
| 185 | 190 | 195 | 200 | |
| gag aag aag cat aaa gtg aaa act aga gtg ctg aga aaa acc ttg gat | | | | 798 |
| Glu Lys Lys His Lys Val Lys Thr Arg Val Leu Arg Lys Thr Leu Asp | | | | |
| 205 210 215 | | | | |
| cca gct ttt gat gag acc ttt aca ttc tat ggg ata ccc tac acc caa | | | | 846 |
| Pro Ala Phe Asp Glu Thr Phe Thr Phe Tyr Gly Ile Pro Tyr Thr Gln | | | | |
| 220 225 230 | | | | |
| atc caa gaa ttg gcc ttg cac ttc aca att ttg agt ttt gac agg ttt | | | | 894 |
| Ile Gln Glu Leu Ala Leu His Phe Thr Ile Leu Ser Phe Asp Arg Phe | | | | |
| 235 240 245 | | | | |
| tca aga gat gat atc att ggg gaa gtt cta att cct ctc tcg gga att | | | | 942 |
| Ser Arg Asp Asp Ile Ile Gly Glu Val Leu Ile Pro Leu Ser Gly Ile | | | | |
| 250 255 260 | | | | |
| gaa tta tct gaa gga aaa atg tta atg aat aga gag atc atc aag aga | | | | 990 |
| Glu Leu Ser Glu Gly Lys Met Leu Met Asn Arg Glu Ile Ile Lys Arg | | | | |
| 265 270 275 280 | | | | |
| aat gtt agg aag tct tca gga cgg ggt gag tta ctg atc tct ctc tgc | | | | 1038 |
| Asn Val Arg Lys Ser Ser Gly Arg Gly Glu Leu Leu Ile Ser Leu Cys | | | | |
| 285 290 295 | | | | |
| tat cag tcc acc aca aac act cta act gtg gtt gtc tta aaa gct cga | | | | 1086 |
| Tyr Gln Ser Thr Thr Asn Thr Leu Thr Val Val Val Leu Lys Ala Arg | | | | |
| 300 305 310 | | | | |
| cat ctg cct aaa tct gat gtg tcc gga ctt tca gat ccc tat gtc aaa | | | | 1134 |
| His Leu Pro Lys Ser Asp Val Ser Gly Leu Ser Asp Pro Tyr Val Lys | | | | |
| 315 320 325 | | | | |
| gtg aac ctg tac cat gcc aaa aag aga atc tcc aag aag aag act cat | | | | 1182 |
| Val Asn Leu Tyr His Ala Lys Lys Arg Ile Ser Lys Lys Lys Thr His | | | | |
| 330 335 340 | | | | |
| gtg aag aaa tgc acc ccc aat gca gtg ttc aat gag ctg ttt gtc ttt | | | | 1230 |
| Val Lys Lys Cys Thr Pro Asn Ala Val Phe Asn Glu Leu Phe Val Phe | | | | |
| 345 350 355 360 | | | | |
| gat att cct tgt gag ggc ctt gaa gat ata agt gtt gaa ttt ttg gtt | | | | 1278 |
| Asp Ile Pro Cys Glu Gly Leu Glu Asp Ile Ser Val Glu Phe Leu Val | | | | |
| 365 370 375 | | | | |
| ttg gat tct gaa agg ggg tcc cga aat gag gta atc ggg cag tta gtc | | | | 1326 |
| Leu Asp Ser Glu Arg Gly Ser Arg Asn Glu Val Ile Gly Gln Leu Val | | | | |

380

385

390

ttg ggt gca gca gca gaa gga act ggt gga gag cac tgg aaa gag atc 1374
 Leu Gly Ala Ala Ala Glu Gly Thr Gly Gly Glu His Trp Lys Glu Ile
 395 400 405

tgt gac tac ccc agg aga caa att gcc aag tgg cac gtg ctc tgt gat 1422
 Cys Asp Tyr Pro Arg Arg Gln Ile Ala Lys Trp His Val Leu Cys Asp
 410 415 420

ggt tagcatccta gccgtgagtt ggaacttaaa ggtttttact aggcaaggag 1475
 Gly
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aaatcttctt tctttctata ttggattgca agcttgggaa atcaagctac ctttttggtg 1535

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acctcacata agaaccatgg ccttggatta ttactgcct gtcacaagcc tcagtgtggc 2195

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atagaagtgt tttggaagga agcatgggtgt gtgagacagt gtctgttctt ttgtgccagc 3815
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<213> Homo sapiens
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20 25 30

Phe Ala Trp Ile Cys Cys Gln Arg Lys Ser Ser Lys Ser Asn Lys Thr
35 40 45

Pro Pro Tyr Lys Phe Val His Val Leu Lys Gly Val Asp Ile Tyr Pro
50 55 60

Glu Asn Leu Asn Ser Lys Lys Lys Phe Gly Ala Asp Asp Lys Asn Glu
65 70 75 80

Val Lys Asn Lys Pro Ala Val Pro Lys Asn Ser Leu His Leu Asp Leu
85 90 95

Glu Lys Arg Asp Leu Asn Gly Asn Phe Pro Lys Thr Asn Leu Lys Pro
100 105 110

Gly Ser Pro Ser Asp Leu Glu Asn Ala Thr Pro Lys Leu Phe Leu Glu
115 120 125

Gly Glu Lys Glu Ser Val Ser Pro Glu Ser Leu Lys Ser Ser Thr Ser
130 135 140

Leu Thr Ser Glu Glu Lys Gln Glu Lys Leu Gly Thr Leu Phe Phe Ser
145 150 155 160

Leu Glu Tyr Asn Phe Glu Arg Lys Ala Phe Val Val Asn Ile Lys Glu
165 170 175

Ala Arg Gly Leu Pro Ala Met Asp Glu Gln Ser Met Thr Ser Asp Pro
180 185 190

Tyr Ile Lys Met Thr Ile Leu Pro Glu Lys Lys His Lys Val Lys Thr
195 200 205

Arg Val Leu Arg Lys Thr Leu Asp Pro Ala Phe Asp Glu Thr Phe Thr

| 210 | 215 | 220 |
|---|-----|---------|
| Phe Tyr Gly Ile Pro Tyr Thr Gln Ile Gln Glu Leu Ala Leu His Phe | | |
| 225 | 230 | 235 240 |
| Thr Ile Leu Ser Phe Asp Arg Phe Ser Arg Asp Asp Ile Ile Gly Glu | | |
| 245 | 250 | 255 |
| Val Leu Ile Pro Leu Ser Gly Ile Glu Leu Ser Glu Gly Lys Met Leu | | |
| 260 | 265 | 270 |
| Met Asn Arg Glu Ile Ile Lys Arg Asn Val Arg Lys Ser Ser Gly Arg | | |
| 275 | 280 | 285 |
| Gly Glu Leu Leu Ile Ser Leu Cys Tyr Gln Ser Thr Thr Asn Thr Leu | | |
| 290 | 295 | 300 |
| Thr Val Val Val Leu Lys Ala Arg His Leu Pro Lys Ser Asp Val Ser | | |
| 305 | 310 | 315 320 |
| Gly Leu Ser Asp Pro Tyr Val Lys Val Asn Leu Tyr His Ala Lys Lys | | |
| 325 | 330 | 335 |
| Arg Ile Ser Lys Lys Lys Thr His Val Lys Lys Cys Thr Pro Asn Ala | | |
| 340 | 345 | 350 |
| Val Phe Asn Glu Leu Phe Val Phe Asp Ile Pro Cys Glu Gly Leu Glu | | |
| 355 | 360 | 365 |
| Asp Ile Ser Val Glu Phe Leu Val Leu Asp Ser Glu Arg Gly Ser Arg | | |
| 370 | 375 | 380 |
| Asn Glu Val Ile Gly Gln Leu Val Leu Gly Ala Ala Ala Glu Gly Thr | | |
| 385 | 390 | 395 400 |
| Gly Gly Glu His Trp Lys Glu Ile Cys Asp Tyr Pro Arg Arg Gln Ile | | |
| 405 | 410 | 415 |
| Ala Lys Trp His Val Leu Cys Asp Gly | | |
| 420 | 425 | |

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<213> Homo sapiens

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21

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 <222> (1)..(30)
 <223> 3' oligo (3489) Lower Primer

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30

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 <212> PRT
 <213> rat

<220>
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 Val Val Gly Ile Phe Ser Ala Phe Gly Leu Val Phe Thr Val Ser Leu
 20 25 30
 Phe Ala Trp Ile Cys Cys Gln Arg Arg Ser Ala Lys Ser Asn Lys Thr
 35 40 45
 Pro Pro Tyr Lys Phe Val His Val Leu Lys Gly Val Asp Ile Tyr Pro
 50 55 60
 Glu Asn Leu Ser Ser Lys Lys Lys Phe Gly Gly Asp Asp Lys Ser Glu
 65 70 75 80
 Ala Lys Arg Lys Ala Ala Leu Pro Asn Leu Ser Leu His Leu Asp Leu

| 85 | | | | | | | | | | 90 | | | | | 95 | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| Glu | Lys | Arg | Asp | Leu | Asn | Gly | Asn | Phe | Pro | Lys | Thr | Asn | Pro | Lys | Ala | | | | |
| | | | 100 | | | | | 105 | | | | | | 110 | | | | | |
| Gly | Ser | Ser | Ser | Asp | Leu | Glu | Asn | Val | Thr | Pro | Lys | Leu | Phe | Pro | Glu | | | | |
| | | | 115 | | | | 120 | | | | | | 125 | | | | | | |
| Thr | Glu | Lys | Glu | Ala | Val | Ser | Pro | Glu | Ser | Leu | Lys | Ser | Ser | Thr | Ser | | | | |
| | | | 130 | | | | 135 | | | | | | 140 | | | | | | |
| Leu | Thr | Ser | Glu | Glu | Lys | Gln | Glu | Lys | Leu | Gly | Thr | Leu | Phe | Leu | Ser | | | | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | | | | |
| Leu | Glu | Tyr | Asn | Phe | Glu | Lys | Lys | Ala | Phe | Val | Val | Asn | Ile | Lys | Glu | | | | |
| | | | | 165 | | | | | 170 | | | | | 175 | | | | | |
| Ala | Gln | Gly | Leu | Pro | Ala | Met | Asp | Glu | Gln | Ser | Met | Thr | Ser | Asp | Pro | | | | |
| | | | 180 | | | | | 185 | | | | | 190 | | | | | | |
| Tyr | Ile | Lys | Met | Thr | Ile | Leu | Pro | Glu | Lys | Lys | His | Lys | Val | Lys | Thr | | | | |
| | | | 195 | | | | 200 | | | | | | 205 | | | | | | |
| Arg | Val | Leu | Arg | Lys | Thr | Leu | Asp | Pro | Val | Phe | Asp | Glu | Thr | Phe | Thr | | | | |
| | | | 210 | | | | 215 | | | | | 220 | | | | | | | |
| Phe | Tyr | Gly | Val | Pro | Tyr | Pro | His | Ile | Gln | Glu | Leu | Ser | Leu | His | Phe | | | | |
| 225 | | | | | 230 | | | | | 235 | | | | 240 | | | | | |
| Thr | Val | Leu | Ser | Phe | Asp | Arg | Phe | Ser | Arg | Asp | Asp | Val | Ile | Gly | Glu | | | | |
| | | | | 245 | | | | | 250 | | | | | 255 | | | | | |
| Val | Leu | Val | Pro | Leu | Ser | Gly | Ile | Glu | Leu | Ser | Asp | Gly | Lys | Met | Leu | | | | |
| | | | 260 | | | | | 265 | | | | | 270 | | | | | | |
| Met | Thr | Arg | Glu | Ile | Ile | Lys | Arg | Asn | Ala | Lys | Lys | Ser | Ser | Gly | Arg | | | | |
| | | | 275 | | | | 280 | | | | | 285 | | | | | | | |
| Gly | Glu | Leu | Leu | Val | Ser | Leu | Cys | Tyr | Gln | Ser | Thr | Thr | Asn | Thr | Leu | | | | |
| | | | 290 | | | | 295 | | | | | 300 | | | | | | | |
| Thr | Val | Val | Val | Leu | Lys | Ala | Arg | His | Leu | Pro | Lys | Ser | Asp | Val | Ser | | | | |
| 305 | | | | | 310 | | | | | 315 | | | | 320 | | | | | |
| Gly | Leu | Ser | Asp | Pro | Tyr | Val | Lys | Val | Asn | Leu | Tyr | His | Ala | Lys | Lys | | | | |
| | | | | 325 | | | | | 330 | | | | 335 | | | | | | |
| Arg | Ile | Ser | Lys | Lys | Lys | Thr | His | Val | Lys | Lys | Cys | Thr | Pro | Asn | Ala | | | | |

| | | |
|---|-----|---------|
| 340 | 345 | 350 |
| Val Phe Asn Glu Leu Phe Val Phe Asp Ile Pro Cys Glu Ser Leu Glu | | |
| 355 | 360 | 365 |
| Glu Ile Ser Val Glu Phe Leu Val Leu Asp Ser Glu Arg Gly Ser Arg | | |
| 370 | 375 | 380 |
| Asn Glu Val Ile Gly Arg Leu Val Leu Gly Ala Thr Ala Glu Gly Ser | | |
| 385 | 390 | 395 400 |
| Gly Gly Gly His Trp Lys Glu Ile Cys Asp Phe Pro Arg Arg Gln Ile | | |
| 405 | 410 | 415 |
| Ala Lys Trp His Met Leu Cys Asp Gly | | |
| 420 | 425 | |

<210> 6
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 <212> PRT
 <213> Homo sapiens

<220>
 <221> PEPTIDE
 <222> (1)..(117)
 <223> PKC-C2 internal repeat (amino acid positions
 154-271)

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| 1 5 10 15 |
| Arg Ile Tyr Leu Glu Ile Asn Val Lys Glu Asn Leu Leu Thr Val Gln |
| 20 25 30 |
| Ile Lys Glu Gly Arg Asn Leu Ile Pro Met Asp Pro Asn Gly Leu Ser |
| 35 40 45 |
| Asp Pro Tyr Val Lys Val Lys Leu Ile Pro Asp Asp Lys Asp Gln Ser |
| 50 55 60 |
| Lys Lys Lys Thr Arg Thr Thr Lys Ala Cys Leu Asn Pro Val Trp Asn |
| 65 70 75 80 |
| Glu Thr Leu Thr Tyr Asp Leu Lys Pro Glu Asp Lys Asp Arg Arg Ile |
| 85 90 95 |

Leu Ile Glu Val Trp Asp Trp Asp Arg Thr Ser Arg Asn Asp Phe Met
100 105 110

Gly Ala Leu Ser Phe
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<210> 7
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<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1)..(121)
<223> Repro-PC-1.0 (PC-20) "B" internal repeat (amino
acid) positions 276-397

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Glu Ile Ile Lys Arg Asn Val Arg Lys Ser Ser Gly Arg Gly Glu Leu
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Leu Ile Ser Leu Cys Tyr Gln Ser Thr Ile Asn Thr Leu Thr Val Val
20 25 30

Val Leu Lys Ala Arg His Leu Pro Lys Ser Asp Val Ser Gly Leu Ser
35 40 45

Asp Pro Tyr Val Lys Val Asn Leu Tyr His Ala Lys Lys Arg Ile Ser
50 55 60

Lys Lys Lys Thr His Val Lys Lys Cys Thr Pro Asn Ala Val Phe Asn
65 70 75 80

Glu Leu Phe Val Phe Asp Ile Pro Cys Glu Gly Leu Glu Asp Ile Ser
85 90 95

Val Glu Phe Leu Val Leu Asp Ser Glu Arg Gly Ser Arg Asn Glu Val
100 105 110

Ile Gly Gln Leu Val Leu Gly Ala Ala
115 120

<210> 8
<211> 115
<212> PRT
<213> rat

<220>

<221> PEPTIDE

<222> (1)..(115)

<223> synaptotagmin "B" internal repeat (amino acid
positions 268-383)

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1 5 10 15

Val Pro Thr Ala Gly Lys Leu Thr Val Val Ile Leu Glu Ala Lys Asn
20 25 30

Leu Lys Lys Met Asp Val Gly Gly Leu Ser Asp Pro Tyr Val Lys Ile
35 40 45

His Leu Met Gln Asn Gly Lys Arg Leu Lys Lys Lys Lys Thr Thr Ile
50 55 60

Lys Lys Asn Thr Leu Asn Pro Tyr Tyr Asn Glu Ser Phe Ser Phe Glu
65 70 75 80

Val Pro Phe Glu Gln Ile Gln Lys Val Gln Val Val Val Thr Val Leu
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Asp Tyr Asp Lys Ile Gly Lys Asn Asp Ala Ile Gly Lys Val Phe Val
100 105 110

Gly Tyr Asn
115

<210> 9

<211> 120

<212> PRT

<213> rat

<220>

<221> PEPTIDE

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<223> synaptotagmin "A" internal repeat (amino acid
positions 134-254)

<400> 9

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Leu Asp Tyr Asp Phe Gln Asn Asn Gln Leu Leu Val Gly Ile Ile Gln
20 25 30

Ala Ala Glu Leu Pro Ala Leu Asp Met Gly Gly Thr Ser Asp Pro Tyr
35 40 45

Val Lys Val Phe Leu Leu Pro Asp Lys Lys Lys Lys Phe Glu Thr Lys
50 55 60

Val His Arg Lys Thr Leu Asn Pro Val Phe Asn Glu Gln Phe Thr Phe
65 70 75 80

Lys Val Pro Tyr Ser Glu Leu Gly Gly Lys Thr Leu Val Met Ala Val
85 90 95

Tyr Asp Phe Asp Arg Phe Ser Lys His Asp Ile Ile Gly Glu Phe Lys
100 105 110

Val Pro Met Asn Thr Val Asp Phe
115 120

<210> 10

<211> 113

<212> PRT

<213> Homo sapiens

<220>

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<223> Repro=PC-1.0 (PC-20) "A" internal repeat amino
acid positions 150-263)

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Glu Arg Lys Ala Phe Val Val Asn Ile Lys Glu Ala Arg Gly Leu Pro
20 25 30

Ala Met Asp Glu Gln Ser Met Thr Ser Asp Pro Tyr Ile Lys Met Thr
35 40 45

Ile Leu Pro Glu Lys Lys His Lys Val Lys Thr Arg Val Leu Arg Lys
50 55 60

Thr Leu Asp Pro Ala Phe Asp Glu Thr Phe Thr Phe Tyr Gly Ile Pro
65 70 75 80

Tyr Thr Gln Ile Gln Glu Leu Ala Leu His Phe Thr Ile Leu Ser Phe
85 90 95

Asp Arg Phe Ser Arg Asp Asp Ile Ile Gly Glu Val Leu Ile Pro Leu
100 105 110

Ser

<210> 11
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<223> residue 1=Thr, Ser or Met

<220>
<223> residue 2=Asp, Glu, Ala, Ser or Thr

<220>
<223> residues 3-8=unknown

<400> 11
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr
1 5

<210> 12
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<212> PRT
<213> Homo sapiens

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<223> residue 1=Thr, Ser or Met

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<223> residue 2=Asp, Glu, Ala, Ser or Thr

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<223> residues 3-9=unknown

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<210> 13
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<213> Homo sapiens

<220>
<223> residue 1=Glu or Asp

<220>
<223> residues 2-6=unknown

<400> 13
Xaa Xaa Xaa Xaa Xaa Xaa Tyr
1 5

<210> 14
<211> 8
<212> PRT
<213> Homo sapiens

<220>
<223> residue 1=Glu or Asp

<220>
<223> residues 2-7=unknown

<400> 14
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr
1 5

<210> 15
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<223> residue 2=Leu, Met, Ile, Val, Ser, Ala, Thr, Phe,
Cys, Gly, Asp or Glu

<220>
<223> residue 9=Lys, Arg or Tyr

<220>
<223> residues 1, 3-8=unknown

<400> 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

1

5

<210> 16

<211> 10

<212> PRT

<213> Homo sapiens

<220>

<223> residue 2= Leu, Met, Ile, Val, Ser, Ala, Thr, Phe,
Cys, Gly, Asp or Glu

<220>

<223> residue 10=Lys, Arg or Tyr

<220>

<223> residues 1,3-9=unknown

<400> 16

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

1

5

10

<210> 17

<211> 9

<212> PRT

<213> Homo sapiens

<220>

<223> residue 2=Thr or Val

<220>

<223> residues 1,3-8=unknown

<400> 17

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys

1

5

<210> 18

<211> 10

<212> PRT

<213> Homo sapiens

<220>

<223> residue 2=Thr or Val

<220>

<223> residues 1,3-10=unknown

<400> 18

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys

1 5 10

<210> 19

<211> 9

<212> PRT

<213> Homo sapiens

<220>

<223> residue 2=Tyr, Phe or Trp

<220>

<223> residue 9=Phe, Ile, Trp, Met or Leu

<220>

<223> residues 1,3-8=unknown

<400> 19

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

1 5

<210> 20

<211> 10

<212> PRT

<213> Homo sapiens

<220>

<223> residue 2=Tyr, Phe or Trp

<220>

<223> residues 1,3-10=unknown

<400> 20

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

1 5 10

<210> 21

<211> 31

<212> PRT

<213> Homo sapiens

<400> 21

Glu Glu Phe Asp Glu Ile Pro Thr Val Val Gly Ile Phe Ser Ala Phe
1 5 10 15

Gly Leu Val Phe Thr Val Ser Leu Phe Ala Trp Ile Cys Cys Gln
20 25 30

<210> 22

<211> 34

<212> PRT

<213> Homo sapiens

<400> 22

Ser Ser Lys Ser Asn Lys Thr Pro Pro Tyr Lys Phe Val His Val Leu
1 5 10 15

Lys Gly Val Asp Ile Tyr Pro Glu Asn Leu Asn Ser Lys Lys Lys Phe
20 25 30

Gly Ala

<210> 23

<211> 25

<212> PRT

<213> Homo sapiens

<400> 23

Ser Pro Ser Asp Leu Glu Asn Ala Thr Pro Lys Leu Phe Leu Glu Gly
1 5 10 15

Glu Lys Glu Ser Val Ser Pro Glu Ser
20 25

<210> 24

<211> 60

<212> PRT

<213> Homo sapiens

<400> 24

Leu Pro Glu Lys Lys His Lys Val Lys Thr Arg Val Leu Arg Lys Thr
1 5 10 15

Leu Asp Pro Ala Phe Asp Glu Thr Phe Thr Phe Tyr Gly Ile Pro Tyr

20

25

30

Thr Gln Ile Gln Glu Leu Ala Leu His Phe Thr Ile Leu Ser Phe Asp
35 40 45

Arg Phe Ser Arg Asp Asp Ile Ile Gly Glu Val Leu
50 55 60

<210> 25

<211> 46

<212> PRT

<213> Homo sapiens

<400> 25

Ile Pro Leu Ser Gly Ile Glu Leu Ser Glu Gly Lys Met Leu Met Asn
1 5 10 15

Arg Glu Ile Ile Lys Arg Asn Val Arg Lys Ser Ser Gly Arg Gly Glu
20 25 30

Leu Leu Ile Ser Leu Cys Tyr Gln Ser Thr Thr Asn Thr Leu
35 40 45

<210> 26

<211> 32

<212> PRT

<213> Homo sapiens

<400> 26

Val Leu Asp Ser Glu Arg Gly Ser Arg Asn Glu Val Ile Gly Gln Leu
1 5 10 15

Val Leu Gly Ala Ala Ala Glu Gly Thr Gly Gly Glu His Trp Lys Glu
20 25 30

<210> 27

<211> 6

<212> PRT

<213> Homo sapiens

<220>

<223> residue 5=Val or Ile

<400> 27

Ser Asp Pro Tyr Xaa Lys

1

5